



#4

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<110> Johansen, Teit E.  
Wen-Yee Saw, Dinah

<120> Novel Neurotrophic Factors

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<140> U.S.S.N 09/804,615

<141> 2001-03-12

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<151> 1998-07-06

<150> USSN 60/092,229

<151> 1998-07-09

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<151> 1998-08-19

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<151> 1999-07-02

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tccccaagcc cacctgggtg ccctctttct ccctgaggct ccacttggtc tctccgcgc 119

atg cct gcc ctg tgg ccc acc ctg gcc gct ctg gct ctg ctg agc agc 167

Met Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu Leu Ser Ser

-95

-90

-85

-80

gtc gca gag gcc tcc ctg ggc tcc gcg ccc cgc agc cct gcc ccc cgc	215
Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg	
-75 -70 -65	
gaa ggc ccc ccg cct gtc ctg gcg tcc ccc gcc ggc cac ctg ccg ggg	263
Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly	
-60 -55 -50	
gga cgc acg gcc cgc tgg tgc agt gga aga gcc cgg cgg ccg cgc cgc	311
Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg	
-45 -40 -35	
aga cac ttc tcg gcc cgc gcc ccc gcc gcc tgc acc ccc atc tgc tct	359
Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser	
-30 -25 -20	
tcc ccg cgg gtc cgc gcg gcg cgg ctg ggg ggc cgg gca gcg cgc tcg	407
Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser	
-15 -10 -5 -1 1	
ggc agc ggg ggc gcg ggg tgc cgc ctg cgc tcg cag ctg gtg ccg gtg	455
Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val	
5 10 15	
cgc gcg ctc ggc ctg ggc cac cgc tcc gac gag ctg gtg cgt ttc cgc	503
Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg	
20 25 30	
ttc tgc acc ggc tcc tgc ccg cgc gcg cgc tct cca cac gac ctc agc	551
Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser	
35 40 45	
ctg gcc agc cta ctg ggc gcc ggg gcc ctg cga ccg ccc ccg ggc tcc	599
Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser	
50 55 60 65	
cgg ccc gtc agc cag ccc tgc tgc cga ccc acg cgc tac gaa gcg gtc	647
Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val	
70 75 80	
tcc ttc atg gac gtc aac agc acc tgg aga acc gtg gac cgc ctc tcc	695
Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser	
85 90 95	
gcc acc gcc tgc ggc tgc ctg ggc tgagggctcg ctccagggct ttgcagactg	749
Ala Thr Ala Cys Gly Cys Leu Gly	
100 105	

gacccttacc ggtggctctt cctgcctggg accctcccg c agagtccac tagccagcg 809

cctcagccag ggacgaaggc ctcaaagctg agaggcccct gccggtgggt gatgga 865

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Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly  
-60 -55 -50

Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg  
-45 -40 -35

Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser  
-30 -25 -20

Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser  
-15 -10 -5 -1 1

Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val  
5 10 15

Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg  
20 25 30

Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser  
35 40 45

Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser  
50 55 60 65

Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val  
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Ala Thr Ala Cys Gly Cys Leu Gly

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 <223> DISULFID: Cys107-Cys107 interchain disulfide  
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Met Pro Gly Leu Ile Ser Ala Arg Gly Gln Pro Leu Leu Glu	
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gtc ctt cct ccc caa gcc cac ctg ggt gcc ctc ttt ctc cct gag gct	96
Val Leu Pro Pro Gln Ala His Leu Gly Ala Leu Phe Leu Pro Glu Ala	
-80 -75 -70	
cca ctt ggt ctc tcc gcg cag cct gcc ctg tgg ccc acc ctg gcc gct	144
Pro Leu Gly Leu Ser Ala Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala	
-65 -60 -55	
ctg gct ctg ctg agc agc gtc gca gag gcc tcc ctg ggc tcc gcg ccc	192
Leu Ala Leu Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro	
-50 -45 -40	
cgc agc cct gcc ccc cgc gaa ggc ccc ccg cct gtc ctg gcg tcc ccc	240
Arg Ser Pro Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro	
-35 -30 -25 -20	
gcc ggc cac ctg ccg ggg gga cgc acg gcc cgc tgg tgc agt gga aga	288
Ala Gly His Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg	
-15 -10 -5	
gcc cgg cgg ccg ccg ccg cag cct tct cgg ccc gcg ccc ccg ccg cct	336
Ala Arg Arg Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro	
-1 1 5 10	
gca ccc cca tct gct ctt ccc cgc ggg ggc cgc gcg gcg ccg gct ggg	384
Ala Pro Pro Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly	
15 20 25	

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ggc ccg ggc aac cgc gct cgg gca gcg ggg gcg cgg ggc tgc cgc ctg 432
Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu
30 35 40 45

cgc tcg cag ctg gtg ccg gtg cgc gcg ctc ggc ctg ggc cac cgc tcc 480
Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser
50 55 60

gac gag ctg gtg cgt ttc cgc ttc tgc agc ggc tcc tgc cgc cgc gcg 528
Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala
65 70 75

cgc tct cca cac gac ctc agc ctg gcc agc cta ctg ggc gcc ggg gcc 576
Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala
80 85 90

ctg cga ccg ccc ccg ggc tcc cgg ccc gtc agc cag ccc tgc tgc cga 624
Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg
95 100 105

ccc acg cgc tac gaa gcg gtc tcc ttc atg gac gtc aac agc acc tgg 672
Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp
110 115 120 125

aga acc gtg gac cgc ctc tcc gcc aac ccc tgc ggc tgc ctg ggc 717
Arg Thr Val Asp Arg Leu Ser Ala Asn Pro Cys Gly Cys Leu Gly
130 135 140

tgagggctcg ctccagggct ttgcagactg gacccttacc ggtggctctt cctgcctggg 777

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agaggcccct gccggtgggt gatg 861

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-80 -75 -70

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Gly Leu Ser Ala Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala

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Pro	Ala	Pro	Arg	Glu	Gly	Pro	Pro	Pro	Val	Leu	Ala	Ser	Pro	Ala	Gly
			-30					-25					-20		
His	Leu	Pro	Gly	Gly	Arg	Thr	Ala	Arg	Trp	Cys	Ser	Gly	Arg	Ala	Arg
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Arg	Pro	Pro	Pro	Gln	Pro	Ser	Arg	Pro	Ala	Pro	Pro	Pro	Pro	Ala	Pro
-1	1				5					10					15
Pro	Ser	Ala	Leu	Pro	Arg	Gly	Gly	Arg	Ala	Ala	Arg	Ala	Gly	Gly	Pro
			20						25					30	
Gly	Asn	Arg	Ala	Arg	Ala	Ala	Gly	Ala	Arg	Gly	Cys	Arg	Leu	Arg	Ser
			35					40					45		
Gln	Leu	Val	Pro	Val	Arg	Ala	Leu	Gly	Leu	Gly	His	Arg	Ser	Asp	Glu
		50					55					60			
Leu	Val	Arg	Phe	Arg	Phe	Cys	Ser	Gly	Ser	Cys	Arg	Arg	Ala	Arg	Ser
	65					70				75					
Pro	His	Asp	Leu	Ser	Leu	Ala	Ser	Leu	Leu	Gly	Ala	Gly	Ala	Leu	Arg
	80				85					90					95
Pro	Pro	Pro	Gly	Ser	Arg	Pro	Val	Ser	Gln	Pro	Cys	Cys	Arg	Pro	Thr
				100					105					110	
Arg	Tyr	Glu	Ala	Val	Ser	Phe	Met	Asp	Val	Asn	Ser	Thr	Trp	Arg	Thr
		115						120					125		
Val	Asp	Arg	Leu	Ser	Ala	Asn	Pro	Cys	Gly	Cys	Leu	Gly			
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<223> Wherein Xaa at position 134 designates Asn or Thr,  
and Xaa at position 135 designates Ala or Pro



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Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro  
1 5 10 15

Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly  
20 25 30

Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln  
35 40 45

Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu  
50 55 60

Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro  
65 70 75 80

His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro  
85 90 95

Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg  
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Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val  
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Asp Arg Leu Ser Ala Xaa Xaa Cys Gly Cys Leu Gly  
130 135 140

<210> 6

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<213> Homo sapiens

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<223> Wherein Xaa at position 110 designates Asn or Thr,  
and Xaa at position 111 designates Ala or Pro

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Ala Ala Arg Ala Gly Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala  
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Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly  
20 25 30

Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly  
35 40 45

Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu  
50 55 60

Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser  
65 70 75 80

Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp  
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Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Xaa Xaa Cys  
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Gly Cys Leu Gly  
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<223> Wherein Xaa at position 107 designates Asn or Thr,  
and Xaa at position 108 designates Ala or Pro

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Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His  
20 25 30

Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg  
35 40 45

Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala  
50 55 60

Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys  
65 70 75 80

Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser  
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Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Xaa Xaa Cys Gly Cys Leu  
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Gly

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 atg gaa ctt gga ctt gga ggc ctc tcc acg ctg tcc cac tgc ccc tgg 105  
 Met Glu Leu Gly Leu Gly Gly Leu Ser Thr Leu Ser His Cys Pro Trp  
 -80 -75 -70 -65  
  
 cct agg cgg cag cct gcc ctg tgg ccc acc ctg gcc gct ctg gct ctg 153  
 Pro Arg Arg Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu  
 -60 -55 -50  
  
 ctg agc agc gtc gca gag gcc tcc ctg ggc tcc gcg ccc cgc agc cct 201  
 Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro  
 -45 -40 -35  
  
 gcc ccc cgc gaa ggc ccc ccg cct gtc ctg gcg tcc ccc gcc ggc cac 249  
 Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His  
 -30 -25 -20  
  
 ctg ccg ggg gga cgc acg gcc cgc tgg tgc agt gga aga gcc cgg cgg 297  
 Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg  
 -15 -10 -5 -1  
  
 ccg ccg ccg cag cct tct ccg ccc gcg ccc ccg ccg cct gca ccc cca 345  
 Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro  
 1 5 10 15  
  
 tct gct ctt ccc cgc ggg ggc cgc gcg gcg ccg gct ggg ggc ccg ggc 393  
 Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly  
 20 25 30  
  
 agc cgc gct ccg gca gcg ggg gcg ccg ggc tgc cgc ctg cgc tcg cag 441  
 Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln

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ctg gtg ccg gtg cgc gcg ctc ggc ctg ggc cac cgc tcc gac gag ctg			489
Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu			
50	55	60	
gtg cgt ttc cgc ttc tgc agc ggc tcc tgc cgc cgc gcg cgc tct cca			537
Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro			
65	70	75	80
cac gac ctc agc ctg gcc agc cta ctg ggc gcc ggg gcc ctg cga ccg			585
His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro			
85	90	95	
ccc ccg ggc tcc cgg ccc gtc agc cag ccc tgc tgc cga ccc acg cgc			633
Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg			
100	105	110	
tac gaa gcg gtc tcc ttc atg gac gtc aac agc acc tgg aga acc gtg			681
Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val			
115	120	125	
gac cgc ctc tcc gcc acc gcc tgc ggc tgc ctg ggc tgagggctcg			727
Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly			
130	135	140	
ctccaggggt ttgcagactg gacccttacc ggtggctctt cctgcctggg accctccgc			787
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Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro			
-45	-40	-35	

Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His  
 -30 -25 -20

Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg  
 -15 -10 -5 -1

Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro  
 1 5 10 15

Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly  
 20 25 30

Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln  
 35 40 45

Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu  
 50 55 60

Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro  
 65 70 75 80

His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro  
 85 90 95

Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg  
 100 105 110

Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val  
 115 120 125

Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly  
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 20 25 30

Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln  
 35 40 45

Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu  
 50 55 60

Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro  
 65 70 75 80

His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro  
 85 90 95

Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg  
 100 105 110

Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val  
 115 120 125

Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly  
 130 135 140

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Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly  
 20 25 30

Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly  
 35 40 45

Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu  
 50 55 60

Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser  
65 70 75 80

Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp  
85 90 95

Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys  
100 105 110

Gly Cys Leu Gly  
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20 25 30

Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg  
35 40 45

Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala  
50 55 60

Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys  
65 70 75 80

Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser  
85 90 95

Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu  
100 105 110

Gly



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 ccgggtccc ggccgatcag ccagccctgc tgccggccca ctgctatga ggccgtctcc 180  
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 <222> (975)..(1646)

<400> 15  
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 tggggtcttc tccaaatgtc tagccccac ctagaggagc ctagcctagc cagcggggac 120  
 cgcatccgga ggggtggagcg gccaggtagg ccctgaaagg tggggcgggg cgggggcgct 180  
 ctgggcccga ccccgggatc tggtagcgcc ggggctggaa tttgacaccg gacggcgggc 240  
 ggcaggaggc tgctgaggga tggagttggg ctcgcccccc agatgcggcc cgcgggctct 300  
 gccagcaaca agtccctcgg gcccagccc tcgctgcgac tggggcttgg agccctgcac 360  
 ccaagggcac agaccggctg ccaaggcccc acttttaact aaaagaggcg ctgccagggtg 420

cacaactctg ggcgatgatcc acttgagctt cgggggaaaag cccagcactg gtcccaggag 480  
 aggcgcctag aaggacacgg accaggaccc ctttggtatg gagtgaacgc tgagcatgga 540  
 gtggaaggaa ctcaagttac tacttttctcc aaccaccctg gtaccttcag ccctgaagta 600  
 cagagcagaa ggggtcttaga agacaggacc acagctgtgt gagtctcccc cctgaggcct 660  
 tagacgatct ctgagctcag ctgagctttg tttgcccatac tggagaagtg agccattgat 720  
 tgaccttggtg gcatcgcgaa ggaacaggtc ctgccaagca cctaacacag agagcaaggt 780  
 tctccatcgc agctaccgct gctgagttga ctctagctac tccaacctcc tgggtcgctt 840  
 cgagagactg gagtggaagg aggaataccc caaaggataa ctaactcatc tttcagtttg 900  
 caagctgccg caggaagagg gtggggaaac ggggtccacga aggcttctga tgggagcttc 960  
 tggagccgaa agct atg gaa ctg gga ctt gca gag cct act gca ttg tcc 1010  
                   Met Glu Leu Gly Leu Ala Glu Pro Thr Ala Leu Ser  
                   1                                  5                                  10  
 cac tgc ctc cgg cct agg tgg cag tca gcc tgg tgg cca acc cta gct 1058  
 His Cys Leu Arg Pro Arg Trp Gln Ser Ala Trp Trp Pro Thr Leu Ala  
                   15                                  20                                  25  
 gtt cta gcc ctg ctg agc tgc gtc aca gaa gct tcc ctg gac cca atg 1106  
 Val Leu Ala Leu Leu Ser Cys Val Thr Glu Ala Ser Leu Asp Pro Met  
                   30                                  35                                  40  
 tcc cgc agc ccc gcc gct cgc gac ggt ccc tca ccg gtc ttg gcg ccc 1154  
 Ser Arg Ser Pro Ala Ala Arg Asp Gly Pro Ser Pro Val Leu Ala Pro  
                   45                                  50                                  55                                  60  
 ccc acg gac cac ctg cct ggg gga cac act gcg cat ttg tgc agc gaa 1202  
 Pro Thr Asp His Leu Pro Gly Gly His Thr Ala His Leu Cys Ser Glu  
                   65                                  70                                  75  
 aga acc ctg cga ccc ccg cct cag tct cct cag ccc gca ccc ccg ccg 1250  
 Arg Thr Leu Arg Pro Pro Pro Gln Ser Pro Gln Pro Ala Pro Pro Pro  
                   80                                  85                                  90  
 cct ggt ccc gcg ctc cag tct cct ccc gct gcg ctc cgc ggg gca cgc 1298  
 Pro Gly Pro Ala Leu Gln Ser Pro Pro Ala Ala Leu Arg Gly Ala Arg  
                   95                                  100                                  105  
 gcg gcg cgt gca gga acc ccg agc agc cgc gca ccg acc aca gat gcg 1346  
 Ala Ala Arg Ala Gly Thr Arg Ser Ser Arg Ala Arg Thr Thr Asp Ala



<212> PRT

<213> Murinae gen. sp.

<400> 16

Met Glu Leu Gly Leu Ala Glu Pro Thr Ala Leu Ser His Cys Leu Arg  
1 5 10 15

Pro Arg Trp Gln Ser Ala Trp Trp Pro Thr Leu Ala Val Leu Ala Leu  
20 25 30

Leu Ser Cys Val Thr Glu Ala Ser Leu Asp Pro Met Ser Arg Ser Pro  
35 40 45

Ala Ala Arg Asp Gly Pro Ser Pro Val Leu Ala Pro Pro Thr Asp His  
50 55 60

Leu Pro Gly Gly His Thr Ala His Leu Cys Ser Glu Arg Thr Leu Arg  
65 70 75 80

Pro Pro Pro Gln Ser Pro Gln Pro Ala Pro Pro Pro Pro Gly Pro Ala  
85 90 95

Leu Gln Ser Pro Pro Ala Ala Leu Arg Gly Ala Arg Ala Ala Arg Ala  
100 105 110

Gly Thr Arg Ser Ser Arg Ala Arg Thr Thr Asp Ala Arg Gly Cys Arg  
115 120 125

Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu Gly Leu Gly His Ser  
130 135 140

Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg  
145 150 155 160

Ala Arg Ser Gln His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly  
165 170 175

Ala Leu Arg Ser Pro Pro Gly Ser Arg Pro Ile Ser Gln Pro Cys Cys  
180 185 190

Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr  
195 200 205

Trp Arg Thr Val Asp His Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly  
210 215 220

<210> 17  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 17

cctggccagc ctactggg

18

<210> 18

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 18

aaggagaccg cttcgtagcg

20

<210> 19

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 19

atggaacttg gacttgg

17

<210> 20

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 20

tccatcaccc accggc

16

<210> 21  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 21

ggccaccgct ccgacgag

18

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 22

ggcgggtccac ggttctccag

20

<210> 23

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 23

ccaagccac ctgggtgcc tctttctcc

29

<210> 24

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 24

catcaccac cggcagggc ctctcag

27

<210> 25  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
  
 <400> 25  
 gagcccatgc ccggcctgat ctacgcccga ggaca 35  
  
 <210> 26  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
  
 <400> 26  
 ccctggctga ggccgctggc tagtgggact ctgc 34  
  
 <210> 27  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Hybridization  
 Probe  
  
 <400> 27  
 ncaggtggtc cgtggggggc gccaaagaccg g 31  
  
 <210> 28  
 <211> 16  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR primer  
  
 <400> 28  
 ctaggagccc atgccc 16

<210> 29  
 <211> 351  
 <212> DNA  
 <213> Homo sapiens

<400> 29  
 atgggtggag gaccgggata tcgtgctcgt gcagcaggag cacgtggctg tcgtctgcgt 60  
 tctcaactag tgccgggtgcg tgcactcgga ctgggacacc gttccgacga actagtacgt 120  
 tttcgttttt gttcaggatc ttgtcgtcgt gcacgttctc cgcattgatc atctctagca 180  
 tctctactag gagccggagc actaagaccg ccgccgggat ctagacctgt atctcaacct 240  
 tgttgtagac ctactagata cgaagcagta tctttcatgg acgtaaactc tacatggaga 300  
 accgtagata gactatctgc aaccgcatgt ggctgtctag gatgataata g 351

<210> 30  
 <211> 414  
 <212> DNA  
 <213> Homo sapiens

<400> 30  
 atggggccatc atcatcatca tcatcatcat catcactcga gcggccatat cgacgacgac 60  
 gacaaggctg gaggaccggg atctcgtgct cgtgcagcag gagcacgtgg ctgtcgtctg 120  
 cgttctcaac tagtgccggg gcgtgcactc ggactgggac accgttccga cgaactagta 180  
 cgttttcggt tttgttcagg atcttgctgt cgtgcacgtt ctccgcatga tctatctcta 240  
 gcatctctac taggagccgg agcactaaga ccgccgccgg gatctagacc tgtatctcaa 300  
 ccttggttgta gacctactag atacgaagca gtatctttca tggacgtaaa ctctacatgg 360  
 agaaccgtag atagactatc tgcaaccgca tgtggctgtc taggatgata atag 414

<210> 31  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer

<400> 31  
 aaggaaaaaa gcggccgcca tggaacttgg acttggagg 39

<210> 32  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>



<223> Description of Artificial Sequence: PCR primer

<400> 32

tttttttcctt ggcggccgct cagcccaggc agccgcagg

39

<210> 33

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 33

gagcgagccc tcagcc

16

<210> 34

<211> 224

<212> PRT

<213> Rattus sp.

<400> 34

Met Glu Leu Gly Leu Gly Glu Pro Thr Ala Leu Ser His Cys Leu Arg  
1 5 10 15

Pro Arg Trp Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu  
20 25 30

Leu Ser Ser Val Thr Glu Ala Ser Leu Asp Pro Met Ser Arg Ser Pro  
35 40 45

Ala Ser Arg Asp Val Pro Ser Pro Val Leu Ala Pro Pro Thr Asp Tyr  
50 55 60

Leu Pro Gly Gly His Thr Ala His Leu Cys Ser Glu Arg Ala Leu Arg  
65 70 75 80

Pro Pro Pro Gln Ser Pro Gln Pro Ala Pro Pro Pro Pro Gly Pro Ala  
85 90 95

Leu Gln Ser Pro Pro Ala Ala Leu Arg Gly Ala Arg Ala Ala Arg Ala  
100 105 110

Gly Thr Arg Ser Ser Arg Ala Arg Ala Thr Asp Ala Arg Gly Cys Arg  
115 120 125

Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu Gly Leu Gly His Ser  
 130 135 140

Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg  
 145 150 155 160

Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly  
 165 170 175

Ala Leu Arg Ser Pro Pro Gly Ser Arg Pro Ile Ser Gln Pro Cys Cys  
 180 185 190

Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr  
 195 200 205

Trp Arg Thr Val Asp His Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly  
 210 215 220

<210> 35

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic gene  
 for Neublabin

<400> 35

taccatggct ggaggaccgg gatctcgtgc tcgtgcagca ggagcacgtg gctgtcgtct 60  
 gcgttctcaa ctagtgccgg tgcgtgcact cggactggga caccgttccg acgaactagt 120  
 acgttttcgt ttttgttcag gatcttgctg tcgtgcacgt tctccgcatg atctatctct 180  
 agcatctcta ctaggagccg gagcactaag accgccgccg ggatctagac ctgtatctca 240  
 accttgttgt agacctacta gatacgaagc agtatctttc atggacgtaa actctacatg 300  
 gagaaccgta gatagactat ctgcaaccgc atgtggctgt ctaggatgat aatagggatc 360  
 cggct 365

<210> 36

<211> 365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic gene

for Neublabin

<400> 36

atggtaccga cctcctggcc cttagacacg agcacgtcgt cctcgtgcac cgacagcaga 60  
cgcaagagtt gatcacggcc acgcacgtga gcctgaccct gtggcaaggc tgcttgatca 120  
tgcaaaagca aaaacaagtc cttagaacagc agcacgtgca agaggcgtac tagatagaga 180  
tcgtagagat gatcctcggc ctcgtgattc tggcggcggc cctagatctg gacatagagt 240  
tggaacaaca tctggatgat ctatgcttcg tcatagaaag tacctgcatt tgagatgtac 300  
ctcttggcat ctatctgata gacgttggcg tacaccgaca gatcctacta ttatccctag 360  
gccga 365

<210> 37

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
Neublabin

<400> 37

Met Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly  
1 5 10 15  
Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly  
20 25 30  
His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys  
35 40 45  
Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly  
50 55 60  
Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro  
65 70 75 80  
Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn  
85 90 95  
Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys  
100 105 110  
Leu Gly

<210> 38

<211> 442  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:synthetic gene  
 gene for HIsNeublastin

<400> 38  
 taccatgggc catcatcatc atcatcatca tcatcatcac tcgagcggcc atatcgacga 60  
 cgacgacaag gctggaggac cgggatctcg tgctcgtgca gcaggagcac gtggctgtcg 120  
 tctgcgttct caactagtgc cggcgcgtgc actcggactg ggacaccgtt ccgacgaact 180  
 agtacgtttt cgtttttgtt caggatcttg tcgtcgtgca cgttctccgc atgatctatc 240  
 tctagcatct ctactaggag ccggagcact aagaccgccg ccgggatcta gacctgtatc 300  
 tcaaccttgt tgtagacctc ctagatacga agcagtatct ttcattggacg taaactctac 360  
 atggagaacc gtagatagac tatctgcaac cgcattgtggc tgtctaggat gataataggg 420  
 atccggctgc taacaaagcc cg 442

<210> 39  
 <211> 442  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:synthetic gene  
 for HisNeublastin

<400> 39  
 atggtacccg gtagtagtag tagtagtagt agtagtagtg agctcgccgg tatagctgct 60  
 gctgctgttc cgacctctg gccctagagc acgagcacgt cgtcctcgtg caccgacagc 120  
 agacgcaaga gttgatcacg gccacgcacg tgagcctgac cctgtggcaa ggctgcttga 180  
 tcatgcaaaa gcaaaaacaa gtcctagaac agcagcacgt gcaagaggcg tactagatag 240  
 agatcgtaga gatgatcctc ggcctcgtga ttctggcggc ggccctagat ctggacatag 300  
 agttggaaca acatctggat gatctatgct tcgtcataga aagtacctgc atttgagatg 360  
 tacctcttgg catctatctg atagacgttg gcgtacaccg acagatccta ctattatccc 420  
 taggcccagc attgtttcgg gc 442

<210> 40  
 <211> 135  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:synthetic  
 HisNeublastin

<400> 40

Met Gly His His His His His His His His His His Ser Ser Gly His  
1 5 10 15

Ile Asp Asp Asp Asp Lys Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala  
20 25 30

Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg  
35 40 45

Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe  
50 55 60

Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu  
65 70 75 80

Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg  
85 90 95

Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser  
100 105 110

Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala  
115 120 125

Thr Ala Cys Gly Cys Leu Gly  
130 135